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RAW SEQUENCE LISTING

DATE: 01/08/2002

PATENT APPLICATION: US/09/963,896

TIME: 10:35:55

Input Set : N:\Crf3\RULE60\09963896.raw

Output Set: N:\CRF3\01082002\I963896.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Lal, Preeti

7 Guegler, Karl J.

8 Corley, Neil C.

10 (ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

13 (iii) NUMBER OF SEQUENCES: 7

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

17 (B) STREET: 3174 PORTER DRIVE

18 (C) CITY: PALO ALTO

19 (D) STATE: CALIFORNIA

20 (E) COUNTRY: USA

21 (F) ZIP: 94304

24 (v) COMPUTER READABLE FORM:

25 (A) MEDIUM TYPE: Floppy disk

26 (B) COMPUTER: IBM PC compatible

27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

28 (D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/09/963,896

C--> 33 (B) FILING DATE: 26-Sep-2001

34 (C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 09/397,558

38 (B) FILING DATE:

40 (viii) ATTORNEY/AGENT INFORMATION:

41 (A) NAME: CERRONE, MICHAEL C.

42 (B) REGISTRATION NUMBER: 39,132

43 (C) REFERENCE/DOCKET NUMBER: PF-0527 US

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (650) 855-0555

48 (B) TELEFAX: (650) 845-4166

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 141 amino acids

56 (B) TYPE: amino acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

60 (vii) IMMEDIATE SOURCE:

61 (A) LIBRARY: PROSTUT10

62 (B) CLONE: 1691243

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

66 Met Val His Val Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser

67 5 10 15

68 Glu Arg Tyr Leu Phe Leu Asn Met Ala Tyr Gln Gln Val His Ala

69 20 25 30

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70 Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu Val Trp Arg Ile Glu
71                               35                               40                               45
72 Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu Ser Leu
73                               50                               55                               60
74 Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp
75                               65                               70                               75
76 Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu
77                               80                               85                               90
78 Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala
79                               95                               100                              105
80 Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe Val
81                               110                              115                              120
82 Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln
83                               125                              130                              135
84 Leu Cys Arg Tyr Pro Asp
85                               140
90 (2) INFORMATION FOR SEQ ID NO: 2:
92   (i) SEQUENCE CHARACTERISTICS:
93       (A) LENGTH: 410 amino acids
94       (B) TYPE: amino acid
95       (C) STRANDEDNESS: single
96       (D) TOPOLOGY: linear
98   (vii) IMMEDIATE SOURCE:
99       (A) LIBRARY: BRSTTUT03
100      (B) CLONE: 1999442
102   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :
104 Met Phe Leu Pro Val Val Leu Ala Ile Arg Ser Arg Tyr Val
105                               5                               10                               15
106 Leu Glu Ala Ala Val Tyr Thr Phe Thr Met Phe Phe Ser Thr Phe
107                               20                               25                               30
108 Tyr His Ala Cys Asp Gln Pro Gly Ile Val Val Phe Cys Ile Met
109                               35                               40                               45
110 Asp Tyr Asp Val Leu Gln Phe Cys Asp Phe Leu Gly Ser Leu Met
111                               50                               55                               60
112 Ser Val Trp Val Thr Val Ile Ala Met Ala Arg Leu Gln Pro Val
113                               65                               70                               75
114 Val Lys Gln Val Leu Tyr Leu Leu Gly Ala Met Leu Leu Ser Met
115                               80                               85                               90
116 Ala Leu Gln Leu Asp Arg His Gly Leu Trp Asn Leu Leu Gly Pro
117                               95                               100                              105
118 Ser Leu Phe Ala Leu Gly Ile Leu Ala Thr Ala Trp Thr Val Arg
119                               110                              115                              120
120 Ser Val Arg Arg Arg His Cys Tyr Pro Pro Thr Trp Arg Arg Trp
121                               125                              130                              135
122 Leu Phe Tyr Leu Cys Pro Gly Ser Leu Ile Ala Gly Ser Ala Val
123                               140                              145                              150
124 Leu Leu Tyr Ala Phe Val Glu Thr Arg Asp Asn Tyr Phe Tyr Ile
125                               155                              160                              165
126 His Ser Ile Trp His Met Leu Ile Ala Gly Ser Val Gly Phe Leu

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127		170		175		180
128	Leu Pro Pro Arg	Ala Lys Thr Asp His	Gly Val Pro Ser Gly	Ala		
129		185		190		195
130	Arg Ala Arg Gly	Cys Gly Tyr Gln Leu	Cys Ile Asn Glu Gln	Glu		
131		200		205		210
132	Glu Pro Gly Pro	Arg Gly Pro Arg Arg	Gly His Cys Gln Gln	His		
133		215		220		225
134	Leu Cys Gln Leu	Arg Gly Ala Leu Gly	Leu Ala Leu Arg Gly	Tyr		
135		230		235		240
136	Glu Cys Phe Leu	Glu Phe Phe Leu Gly	Val Trp Ser Pro Leu	Arg		
137		245		250		255
138	Arg Arg Gln Ala	Val Phe Leu Glu Asp	Met Glu Ser Phe Ser	Arg		
139		260		265		270
140	Thr Gln Asn Ser	Ser Arg Asp Leu Glu	Pro Phe Pro Gly His	Gly		
141		275		280		285
142	Glu Leu Pro Glu	Gly Leu Glu Ser Pro	Cys Ile Met Glu Ser	Phe		
143		290		295		300
144	Leu Arg Thr Gly	Ala Tyr Ala Gly Thr	Glu Ser Leu Arg Thr	Lys		
145		305		310		315
146	Glu Ser Leu Leu	Gln Val Trp Ser Leu	Ser Trp Asp Ala Glu	Pro		
147		320		325		330
148	Ser Gln Asp Met	Asp Ser Phe Pro Gly	Arg Gln Ser Pro Val	Arg		
149		335		340		345
150	Ser Thr Ala Ser	Phe Gln Arg Arg Trp	Ser Leu Ser Trp Gly	Asn		
151		350		355		360
152	Gln Ile Ser Arg	Phe Ser Gln Arg Leu	Ser Asn Ser Gly Leu	Arg		
153		365		370		375
154	Leu Pro Ser Gln	Arg Gln Arg Leu Gly	Cys Ala Val Leu Trp	Arg		
155		380		385		390
156	Arg Asp Cys Arg	Met Asp Gly Ala Gly	Thr Gly Ala Val Trp	Val		
157		395		400		405
158	Ala Gly Ile Leu	Val				
159		410				

164 (2) INFORMATION FOR SEQ ID NO: 3:

166 (i) SEQUENCE CHARACTERISTICS:

167 (A) LENGTH: 1213 base pairs

168 (B) TYPE: nucleic acid

169 (C) STRANDEDNESS: single

170 (D) TOPOLOGY: linear

172 (vii) IMMEDIATE SOURCE:

173 (A) LIBRARY: PROSTUT10

174 (B) CLONE: 1691243

176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

178	CAAGTATAGG AGATTTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG	60
179	ATTACTAAGT TTTTCTTCG CTATGGTCCA TGTTGCCTAC AGCCTCTGCT TACCGATGAG	120
180	AAGGTCAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTTTCATG CAAATATTGA	180
181	AAACTCTTGG AATGAGGAAG AAGTTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT	240
182	GAGCCTTGGC TTACTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT	300
183	AAACTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG	360

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184 TACTTTCCAT GTTTTAATTT ATGGATGGAA ACGAGCTTTT GAGGAAGAGT ACTACAGATT 420
185 TTATACACCA CCAAACCTTG TTCTTGCTCT TGTTTTGCCC TCAATTGTAA TTCTGGATCT 480
186 TTTGCAGCTT TGCAGATACC CAGACTGAGC TGGAACCTGA ATTTGTCTTC CTATTGACTC 540
187 TACTTCTTTA AAAGCGGCTG CCCATTACAT TCCTCAGCTG TCCTTGCACT TAGGTGTACA 600
188 TGTGACTGAG TGTTGGCCAG TGAGATGAAG TCTCCTCAAA GGAAGGCAGC ATGTGTCCTT 660
189 TTTCATCCCT TCATCTTGCT GCTGGGATTG TGGATATAAC AGGAGCCCTG GCAGCTGTCT 720
190 CCAGAGGATC AAAGCCACAC CCAAAGAGTA AGGCAGATTA GAGACCAGAA AGACCTTGAC 780
191 TACTTCCCTA CTTCCACTGC TTTTCTCCTT ATTTAAGCCA TTGTAAATCT GGGTGTGTTA 840
192 CATGAAGTGA AAATTAATTC TTTCTGCCCT TCAGTTCTTT ATCCTGATAC CATTTAACAC 900
193 TGTCTGAATT AACTAGACTG CAATAATTCT TTCTTTTGAA AGCTTTTAAA GGATAATGTG 960
194 CAATTCACAT TAAAATTGAT TTTCCATTGT CAATTAGTTA TACTCATTTT CCTGCCTTGA 1020
195 TCTTTCATTA GATATTTTGT ATCTGCTTGG AATATATTAT CTCTTTTTA ACTGTGTAAT 1080
196 TGGTAATTAC TAAAACCTCTG TAATCTCCAA AATATTGCTA TCAAATTACA CACCATGTTT 1140
197 TCTATCATTC TCATAGATCT GCCTTATAAA CATTTAAATA AAAAGTACTA TTTAATGATT 1200
198 TAAAAAAAAA AAA 1213
201 (2) INFORMATION FOR SEQ ID NO: 4:
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 1297 base pairs
205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear
209 (vii) IMMEDIATE SOURCE:
210 (A) LIBRARY: BRSTTUT03
211 (B) CLONE: 1999442
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :
215 CGGACGCGTG GGCTGCTCTG CCTGAGCAAC CTCATGTTTC TGCCACCTGT GGTCTCTGGCC 60
216 ATTCGAGAGT GATATGTGCT GGAAGCTGCA GTCTACACCT TCACCATGTT CTTCTCCACG 120
217 TTCTATCATG CCTGTGACCA GCCAGGCATC GTGGTTTTCT GCATCATGGA CTACGATGTG 180
218 CTGCAGTTCT GTGATTTTCT GGGCTCCTTA ATGTCCGTGT GGGTCACTGT CATTGCCATG 240
219 GCTCGTTTAC AGCCCGTGGT CAAGCAGGTG CTGTATTTGC TGGGAGCTAT GCTGCTGTCC 300
220 ATGGCTCTGC AGCTTGACCG ACATGGACTC TGGAACCTGC TTGGACCCAG TCTCTTCGCC 360
221 CTGGGGATCT TGGCCACAGC CTGGACAGTA CGCAGCGTCC GCCGCCGGCA CTGCTACCCA 420
222 CCCACGTGGC GCCGCTGGCT TTTCTACTTG TGCCCTGGCA GCCTTATTGC AGGCAGTGCC 480
223 GTCCTGCTTT ATGCTTTTGT GGAGACCCGG GACAACTACT TCTACATTCA CAGCATTTGG 540
224 CATATGCTCA TTGCGGGCAG TGTGGGCTTC CTGCTGCCCC CTCGTGCCAA GACTGACCAC 600
225 GGGGTCCCAT CTGGAGCCCG GGCCCGGGGC TGTGGTTACC AGCTATGCAT CAACGAGCAG 660
226 GAGGAGCCTG GGCTCGTGG GCCCAGGAGG GGCCACTGTC AGCAGCATCT GTGCCAGCTG 720
227 AGAGGGGCTT TGGGCCTGGC CCTGAGGGGA TATGAATGCT TCCTAGAGTT CTTTCTGGGG 780
228 GTGTGGAGCC CTCTTAGAAG GAGACAGGCT GTATTTCTTG AGGACATGGA GTCTTTCTCA 840
229 AGGACACAAA ACTCTTCCAG GGACCTGGAG CCCTTCCCAG GACATGGAGA ACTTCCTGAG 900
230 GGCCTGGAGT CCCCCTGCAT CATGGAGTCC TTCTTAAGGA CTGGAGCCTA TGCAGGCACA 960
231 GAGTCCCTCA GGACCAAGGA GTCCCTCCTG CAGGTGTGGA GCCTTTCCTG GGATGCAGAG 1020
232 CCTTCCCAAG ACATGGATTG CTTCCAGGG AGACAAAGCC CTGTCAGGAG CACAGCATCT 1080
233 TTCCAGAGGA GGTGGAGTCT ATCTTGGGGA AACCAAATTT CCAGATTTTC CCAGAGGCTC 1140
234 AGCAACTCTG GCCTCAGGCT TCCTTCCCAG AGGCAGCGTC TGGGCTGTGC TGTGCTGTGG 1200
235 AGGAGGGATT GCAGGATGGA TGGAGCTGGG ACTGGGGCTG TCTGGGTGGC TGGTATCCTC 1260
236 GTTTGATACA GGTGGAGTCT CTGTGTCTCC ATAGAAG 1297
239 (2) INFORMATION FOR SEQ ID NO: 5:
241 (i) SEQUENCE CHARACTERISTICS:

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242 (A) LENGTH: 76 amino acids
 243 (B) TYPE: amino acid
 244 (C) STRANDEDNESS: single
 245 (D) TOPOLOGY: linear
 247 (vii) IMMEDIATE SOURCE:
 248 (A) LIBRARY: GenBank
 249 (B) CLONE: 1216498
 251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :
 253 Met Gly Arg Ala Met Val Val Arg Leu Gly Leu Leu Leu
 254 5 10 15
 255 Leu Ala Leu Leu Leu Pro Thr Gln Ile Tyr Cys Asn Gln Thr Ser
 256 20 25 30
 257 Val Ala Pro Phe Ser Gly Asn Gln Ser Ile Ser Ala Ala Pro Asn
 258 35 40 45
 259 Pro Thr Asn Ala Thr Thr Arg Ser Gly Cys Ser Ser Leu Gln Ser
 260 50 55 60
 261 Thr Ala Gly Leu Leu Ala Leu Ser Leu Ser Leu Leu His Leu Tyr
 262 65 70 75
 263 Cys
 268 (2) INFORMATION FOR SEQ ID NO: 6:
 270 (i) SEQUENCE CHARACTERISTICS:
 271 (A) LENGTH: 261 amino acids
 272 (B) TYPE: amino acid
 273 (C) STRANDEDNESS: single
 274 (D) TOPOLOGY: linear
 276 (vii) IMMEDIATE SOURCE:
 277 (A) LIBRARY: GenBank
 278 (B) CLONE: 130989
 280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :
 282 Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile
 283 5 10 15
 284 Gly Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu
 285 20 25 30
 286 Cys Glu Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg
 287 35 40 45
 288 Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val
 289 50 55 60
 290 Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu
 291 65 70 75
 292 Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val Phe
 293 80 85 90
 294 Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu
 295 95 100 105
 296 Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp
 297 110 115 120
 298 Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala
 299 125 130 135
 300 Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr
 301 140 145 150

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/963,896

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TIME: 10:35:56

Input Set : N:\Crf3\RULE60\09963896.raw

Output Set: N:\CRF3\01082002\I963896.raw

L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]